

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 25.6395 Seconds
(without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613b-6
Perfect score: 583
Sequence: 1 MDWLTFOKKHLTNTRDVC.....TFCVTCENQAPVHFVGCHC 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	99.1	127	13	0918V8
2	556	95.4	127	13	08UVX5
3	404.5	69.4	129	13	09DFY6
4	386	66.2	128	13	09DFY8
5	311	53.3	128	13	09DFY7
6	309	53.0	128	13	09DFY5
7	298	51.1	133	13	098SM0
8	292	50.1	133	13	09PMR7
9	286	49.1	133	13	098SL9
10	285	48.9	133	13	098SM2
11	282	48.4	133	13	098SL8
12	280	48.0	132	13	098SM1
13	275.5	47.3	132	13	09DF78
14	157.5	27.0	169	13	09W738
15	129	22.1	152	11	09JKI5
16	127	21.8	157	11	09JKI9

17	126.5	21.7	153	11	09JKI7	09JKI7 mus saxicol
18	126	21.6	157	11	09JKJ3	09JKJ3 meriones un
19	125	21.4	157	11	09JKJ4	09JKJ4 meriones un
20	123	21.1	154	11	09JKI8	09JKI8 mus saxicol
21	122	20.9	157	11	09JKJ1	09JKJ1 meriones un
22	121	20.8	157	11	09JKJ2	09JKJ2 meriones un
23	120.5	20.7	155	11	09JKI9	09JKI9 mus pahari
24	119.5	20.5	155	11	09JKI3	09JKI3 mus saxicol
25	116.5	20.0	155	11	09JKI6	09JKI6 mus saxicol
26	115.5	19.8	132	6	09TV25	09TV25 eullemur ful
27	115.5	19.8	135	11	09JKI4	09JKI4 mus saxicol
28	115.5	19.8	155	11	09JKI2	09JKI2 mus saxicol
29	114.5	19.6	132	6	09TV24	09TV24 galago moho
30	114.5	19.6	170	6	09BEC1	09BEC1 tragulus ja
31	113.5	19.5	119	6	09TSO6	09TSO6 cercopithec
32	113.5	19.5	119	6	09TV32	09TV32 gorilla gor
33	113.5	19.5	155	11	09RI34	09RI34 ratius norv
34	113	19.4	156	11	09JKH7	09JKH7 mus caroli
35	113	19.4	156	11	09JKG6	09JKG6 bubalus bub
36	112.5	19.3	119	6	09TV30	09TV30 saginus oe
37	112.5	19.3	155	11	09RI25	09RI25 mus musculu
38	112.5	19.3	155	11	09JKH8	09JKH8 mus pahari
39	112	19.2	124	6	09TSE2	09TSE2 bos taurus
40	112	19.2	156	11	09JKG7	09JKG7 mus caroli
41	111.5	19.1	155	11	09JKG3	09JKG3 mus caroli
42	111	19.0	124	6	09SNE6	09SNE6 bubalus bub
43	111	19.0	156	6	08SQ04	08SQ04 lemur calta
44	111	19.0	156	11	09JKH5	09JKH5 mus caroli
45	111	19.0	156	11	09JKH4	09JKH4 mus caroli

ALIGNMENTS

RESULT 1

ID	0918V8	PRELIMINARY:	PRT:	127 AA.
AC	0918V8:			
DT	01-OCT-2000 (TREMBLERel. 15. Created)			
DT	01-OCT-2000 (TREMBLERel. 15, last sequence update)			
DT	01-DEC-2001 (TREMBLERel. 19, last annotation update)			
DE	Onconase variant rap1L precursor.			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RX	MEDLINE=20330357; PubMed=10871370;			
RT	Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.:			
RT	"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a			
RT	3' UTR of unusual length and structure."			
RL	Nucleic Acids Res. 28:2375-2382(2000).			
DR	EMBL; AF165133; AAF76935.1; -			
DR	HSSP; P22069; IONC.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_PC; 1.			
DR	PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL. 1 23 POTENTIAL.			
SO	SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;			
Query Match	99.1%; Score 578; DB 13; Length 127;			
Best Local Similarity	100.0%; Pred. No. 2e-58;			
Matches	104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

OY 2 QDWLTFOKKHLTNTRDVCNNINSTNLFHCKDKKTFIYSRPEPKAKCKGIASKNVLT 61
DB 24 QDWLTFOKKHLTNTRDVCNNINSTNLFHCKDKKTFIYSRPEPKAKCKGIASKNVLT 83

OY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
 DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2

ID Q8UVX5 PRELIMINARY; PRT: 127 AA.
 AC Q8UVX5;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Onconase precursor.
 GN RPR.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NX NCBI_TaxID=8404;

RM SEQUENCE FROM N.A.
 RA Liao Y.-D., Wang S.-C.;
 RT "Rana pipiens onconase genomic DNA."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF332139; AAL54383.1; -
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 95.4%; Score 556; DB 13; Length 127;
 Best Local Similarity 96.2%; Pred. No. 6.5e-56;
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 QDWLTFQKHLJTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAIKGIISKNVLT 61
 DB 24 QDWLTFQKHLJTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAIKGIISKNVLT 83
 OY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
 DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 127

RESULT 3

ID Q9DFY6 PRELIMINARY; PRT: 129 AA.
 AC Q9DFY6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RC-RNase4 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NX NCBI_TaxID=8400;

RM SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RA MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN (12)

RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF242555; AAG31441.2; -
 DR HSSP; P22069; IONC.

DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
 SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 69.4%; Score 404.5; DB 13; Length 129;
 Best Local Similarity 67.6%; Pred. No. 1.4e-38;
 Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 2 QDWLTFQKHLJTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAIKGIISKNVLT 61
 DB 24 QDWLTFQKHLJTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAIKGIISKNVLT 83
 OY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
 DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 127

RESULT 4

ID Q9DFY8 PRELIMINARY; PRT: 128 AA.
 AC Q9DFY8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RC-RNase2 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NX NCBI_TaxID=8400;

RM SEQUENCE FROM N.A.
 RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN (12)

RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF242553; AAG31439.1; -
 DR HSSP; P22069; IONC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 66.2%; Score 386; DB 13; Length 128;
 Best Local Similarity 67.3%; Pred. No. 1.8e-36;
 Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

OY 2 QDWLTFQKHLJTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAIKGIISKNVLT 61
 DB 24 QDWLTFQKHLJTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAIKGIISKNVLT 83
 OY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
 DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 127

ID	Q9DFY7	PRELIMINARY:	PRT:	128 AA.
AC	Q9DFY7;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	RC-RNase3 ribonuclease precursor.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_Taxid=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER.			
RX	MEDLINE=20512555; PubMed=11058105;			
RA	Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;			
RT	"Purification and cloning of cytotoxic ribonucleases from Rana			
RT	catesbeiana (bullfrog)."			
RL	Nucleic Acids Res. 28:4097-4104(2000).			
DR	EMBL; AF242554; AACG1440.2; -.			
DR	HSSP; P22069; IONC.			
DR	InterPro; IPR001427; RNaseA.			
DR	Pfam; PF00074; rnasea; 1.			
DR	ProDom; PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_Fc; 1.			
DR	ProSITE; PS00127; RNase_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL 1 23 POTENTIAL.			
FT	CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.			
SO	SEQUENCE 128 AA; 14517 MW; 2814986082E0587D CAC64;			
Query Match				
Best Local Similarity 53.3%; Score 311; DB 13; Length 128;				
Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0;				
QY	2 QDWTFQKHILTNRDVDCNNIMSTNLFHCCKDKNTFIYSREPPYKAIGKIIASNNVLT 61			
Db	24 IDMTFFQKHILTDKRYKCDVEMAKALFDCKRTNFYIALGRVAKALCKNIRMDTVLSR 83			
QY	62 SEFLSDCNVTSRPCYKYLKSTNTFCVTCENAPVHPVGHG 105			
Db	84 DAFLLPQCDRIKLPCHYKLSSSTNTTICTCVNPILHPAGVGC 127			

ID	Q98SMO	PRELIMINARY:	PRT:	133 AA.
DR	Pfam: PF00074: rnaaseA. 1.			
DR	ProDom: PD000535: rnaaseA. 1.			
DR	SMART: SM00092: RNase_Pc. 1.			
DR	ProSite: PS00127: RNASE_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL			
FT	CHAIN			
SO	SEQUENCE	128 AA; 14804 MW; AEFBF67D266C7C2 CRC64;		
	Query Match	53.0%; Score 309; DB 13; Length 128;		
	Best Local Similarity	53.8%; Pred. No. 1,1e-27;		
	Matches	56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;		
OY	2 QDWLTFQKHLLTNRDVCNNIMSTNLFHCCKDKNTFIYSRPPYKAICGIIASKNVLTT 61			
DB	24 QDWTFQKHLLTDRKVKCDVEMKALFDCKKRTNFIIFARPPVQALCKNIKIDMTNVLRS 83			
OY	62 SEFLSDCQNTVSRPCKYKLRKSTNFEVTCENQAPVHVGVC 105			
DB	84 DVFLPQCNRKKLPCHRLDGSNTVITCLTKMKELPIHPAGVKC 127			
	RESULT 7			
ID	Q98SMO	PRELIMINARY:	PRT:	133 AA.
AC	Q98SMO:			
DT	01-JUN-2001 (TREMBlrel. 17, Created)			
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	RNase A-type, ribonuclease rc208 precursor.			
OS	Rana catesbeiana (Bull Frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21539506; PubMed=11683320;			
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;			
RT	"Rapid diversification of RNase A superfamily ribonuclease from the			
RT	bullfrog, Rana catesbeiana.";			
RL	J. Mol. Evol. 53:31-38(2001).			
DR	EMBL: AF351209; AAK30255.1; -.			
DR	HSSP: P11916; IBC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; rnaaseA. 1.			
DR	ProDom: PD000535; RNaseA. 1.			
DR	SMART: SM00092; RNase_Pc. 1.			
DR	ProSite: PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL			
SO	SEQUENCE	133 AA; 14628 MW; 87FCF12C3499E02 CRC64;		
	Query Match	51.1%; Score 298; DB 13; Length 133;		
	Best Local Similarity	49.5%; Pred. No. 2,1e-26;		
	Matches	55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;		
OY	2 QDWLTFQKHLLTNRDVCNNIMSTNLFHCCKDKNTFIYSRPPYKAICGIIASKNVL 57			
DB	23 QNWATFQCKHTNTSSINCNTIMDNNTIYVGQCGVNTFIISATYTKAICTGVI-RMN 81			
OY	58 VLTTSSEFLSDC---NVTSRPCKYKLRKSTNFEVTCENQAPVHVGVC 105			
DB	82 VLSSTRFQNLNCTRTSITPRCPYSSPRNNNTICVCKCENQVPHVHAGIGRC 132			
	RESULT 8			
ID	Q9PMW7	PRELIMINARY:	PRT:	133 AA.
AC	Q9PMW7:			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	Ribonuclease precursor.			

```

GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Liao Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity."
RL J. Biol. Chem. 273:6395-6401(1998).
DR EMBL: AF039104; AAD10702.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;
Query Match 50.1%; Score 292; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 1e-25;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

OY 2 QDWLTFQKHILTNTRDVDCNNIMSTNLF---HCKDKNFTYSRPEPVKAICKGIASKN 57
DB 23 QWNAFTFOQKHILTNTRDVDCNNIMSTNLF---HCKDKNFTYSRPEPVKAICKGIASKN 57
OY 58 VLTTSSEFYLSDC---NVTSRPCKYKLLKSTNFCVTCENQAPVHFGVGHIC 105
DB 82 VLSSTRFQDLICTRIFITPRCPYSSKRTETNYICVKNENQYPVHFGAGIGRC 132

RESULT 9
O98SL9 ID PRELIMINARY; PRT; 133 AA.
AC O98SL9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351207; AAK30256.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14615 MW; C878B5236B26E54E CRC64;
Query Match 49.1%; Score 286; DB 13; Length 133;
Best Local Similarity 47.7%; Pred. No. 4.9e-25;
Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

```

```

OY 2 QDWLTFQKHILTNTRDVDCNNIMSTNLF---HCKDKNFTYSRPEPVKAICKGIASKN 57
DB 23 QWNAFTFOQKHILTNTRDVDCNNIMSTNLF---HCKDKNFTYSRPEPVKAICKGIASKN 57
OY 58 VLTTSSEFYLSDC---NVTSRPCKYKLLKSTNFCVTCENQAPVHFGVGHIC 105
DB 82 VLSSTRFQDLICTRIFITPRCPYSSKRTETNYICVKNENQYPVHFGAGIGRC 132

RESULT 10
O98SM2 ID PRELIMINARY; PRT; 132 AA.
AC O98SM2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 21, Last annotation update)
DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF351207; AAK30253.1; -.
DR EMBL: AF359578; AAL87036.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;
Query Match 48.9%; Score 285; DB 13; Length 132;
Best Local Similarity 47.7%; Pred. No. 6.3e-25;
Matches 53; Conservative 14; Mismatches 36; Indels 8; Gaps 3;

OY 2 QDWLTFQKHILTNTRDVDCNNIMSTNLF---HCKDKNFTYSRPEPVKAICKGIASKN 57
DB 23 QWNAFTFOQKHILTNTRDVDCNNIMSTNLF---HCKDKNFTYSRPEPVKAICKGIASKN 57
OY 58 VLTTSSEFYLSDC---NVTSRPCKYKLLKSTNFCVTCENQAPVHFGVGHIC 105
DB 82 VLSSTRFQDLICTRIFITPRCPYSSKRTETNYICVKNENQYPVHFGAGIGRC 132

RESULT 11
O98SL8 ID PRELIMINARY; PRT; 133 AA.
AC O98SL8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.

```

RX	MEDLINE21539506; PubMed-11683320;
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D. ;
RT	"Rapid diversification of RNase A superfamily ribonuclease from the
RL	bullfrog, Rana catesbeiana." ;
J.	Mol. Evol. 53:31-38(2001).
DR	EMBL; AF351211; AAC30257.1; .
DR	HSSP; P11916; 1BC4.
DR	InterPro: IPR001427; RNaseA.
DR	Pfam: PF00074; rna5eA; 1.
DR	Prodrom: PD00535; RNaseA; 1.
DR	SMART; SM00092; RNase_Pc; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
FT	SIGNAL
SO	SEQUENCE 133 AA; 14590 MW; 8B40B9A9AFAB9A3 CRC64; POTENTIAL.
QY	Query Match 48.4%; Score 282; DB 13; Length 133; Best Local Similarity 46.8%; Pred. No. 1,4e-24; Matches 52; Conservative 18; Mismatches 33; Indels 8; Gaps 3
Dy	2 QDMLTPOKHLITNRDVDCNNIMSTNLF---HCKDKMTFYISREPYKAICKGIIASKN 57 : : : : : 23 QNAATFPOQHHTNTSSINCINMNSLYIGGGCKKVATFFLAASATYYAKGICSG-VTDKK 81
OY	58 VLTISEEFLSCDN--VTSRPCYKLKSKSTMFVCYCENQAPVHFVGCHC 105 : : : : : 82 VLSTTRPOLXXXTRIFTITSRCPPISSTKETNKICYKCENEPVHFAGIGKC 132
RESULT 12	
O98SM1	PRELIMINARY; PRT; 132 AA.
ID	O98SM1
AC	O98SM1;
DT	01-JUN-2001 (TREMblrel. 17; Created)
DT	01-JUN-2001 (TREMblrel. 17; Last sequence update)
DT	01-DEC-2001 (TREMblrel. 19; last annotation update)
DE	Rnase A-type ribonuclease rc204 precursor.
OS	Rana catesbeiana (Bull frog) .
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Ambiphyla; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX	NCBI_TaxID=8400;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21539506; PubMed=11683320;
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D. ;
RT	"Rapid diversification of RNase A superfamily ribonuclease from the
RL	bullfrog, Rana catesbeiana." ;
J.	Mol. Evol. 53:31-38(2001).
DR	EMBL; AF351208; AAC30254.1; .
DR	HSSP; P11916; 1BC4.
DR	InterPro: IPR001427; RNaseA.
DR	Pfam: PF00074; rna5eA; 1.
DR	Prodrom: PD00535; RNaseA; 1.
DR	SMART; SM00092; RNase_Pc; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
FT	SIGNAL
SO	SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64; POTENTIAL.
QY	Query Match 48.0%; Score 280; DB 13; Length 132; Best Local Similarity 46.6%; Pred. No. 2,4e-24; Matches 54; Conservative 14; Mismatches 35; Indels 8; Gaps 3
Dy	2 QDMLTPOKHLITNRDVDCNNIMSTNLF---HCKDKMTFYISREPYKAICKGIIASKN 57 : : : : : 23 QDMFTFOOKHPTSSISDCNFMPIKDIVRGCGCKVMTFYIYSATYKAICTGVLSN-N 81
OY	58 VLTISEEFLSCDN--VTSRPCYKLKSKSTMFVCYCENQAPVHFVGCHC 105 : : : : : 82 VLSTTRPOLXXXTRIFTITSRCPPISSTKETNKICYKCENEPVHFAGIGKC 132
RESULT 13	

ID	Q9DF78	PRELIMINARY:	PRT:	132 AA.
AC	Q9DF78:			
DT	01-MAR-2001 (TReMBLrel. 16, Created)			
DT	01-OCT-2001 (TReMBLrel. 18, Last sequence update)			
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)			
DE	RC-RNaseL1 ribonuclease precursor.			
OS	Rana catesbeiana (bull frog).			
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
OC	Amphibia: Batrachia: Anura: Neobatrachia: Ranoidae: Ranidae: Rana.			
OX	NCBI_TaxID=8400:			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=LIVER.			
RX	MEDLINE=20512555; PubMed=11058105;			
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.,			
RA	"Purification and cloning of cytotoxic ribonucleases from Rana			
RT	catesbeiana (bullfrog).";			
RL	Nucleic Acids Res. 28:4097-4104(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=LIVER.			
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.,			
RA	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF288642; AAC30414.2; .			
DR	HSSP; P11916; IBC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA: 1.			
DR	ProDom: PD000535; RNaseA: 1.			
DR	SMART: SM00092; RNase_Pc: 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	132	RC-RNASEL1 RIBONUCLEASE.
SO	SEQUENCE	132 AA;	14625 MW;	D8D9A517452FBE53 CRC4;
QY	Query Match	47.38;	Score 275.5;	DB 13; Length 132;
QY	Best Local Similarity	44.18;	Pred. No. 7.7e-24;	
QY	Matches	49;	Conservative 19;	Mismatches 36; Indels 7; Gaps
DB	2 QNMTPCKKHJLNTRDVDCNNIMSTNLF---HCKDKNPFYSRPPVKAICKGIASKN 57			
QY	22 QNMAKFEKHTTSSIDCNTIMDKATIVYGCKCKERNFTLISSEDNVAKISGVSPDK 81			
DB	58 VLTSEFYLSDC--NVTSPKCYKLLKSTNFCVCENQAPVHEGVGHC 105			
QY	82 ELSTTSKLMCTIRDSTTPRCPCYHPSPDNKKICVGCENQLPVPYFGIGKC 132			
RESULT 14				
ID	Q9W738	PRELIMINARY:	PRT:	169 AA.
AC	Q9W738:			
DT	01-NOV-1999 (TReMBLrel. 12, Created)			
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)			
DT	01-JUN-2001 (TReMBLrel. 17, Last annotation update)			
DE	FR12 protein.			
GN	FR12.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
OC	Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae:			
OC	Xenopodinae: Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96069863; PubMed=7585965;			
RA	Kinoshta N., Minshull J., Kirschner M.W.,			
RT	"The identification of two novel ligands of the FGF receptor by a			
RL	yeast screening method and their activity in Xenopus development.";			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Kinoshta N., Kirschner M.W.;			

